IN THE SPECIFICATION:

Please revise the specification as follows:

Please replace the paragraph that bridges pages 14-15, which begins at page 14, line 23, with the following paragraph:

FIG. 37A-C. Binding of phosphorylated p27 to Skp2. **A.** A panel of in vitro translated [35S]FBPs were used in binding reactions with beads coupled to the phospho-peptide NAGSVEQT*PKKPGLRRRQT (SEQ. ID NO: 85), corresponding to the carboxy terminus of the human p27 with a phosphothreonine at position 187 (T*). Beads were washed with RIPA buffer and bound proteins were eluted and subjected to electrophoresis and autoradiography (Upper Panel). Bottom Panel: 10% of the in vitro translated [35S]FBP inputs. **B.** HeLa cell extracts were incubated with beads coupled to the phospho-p27 peptide (lane 2), an identical except unphosphorylated p27 peptide (lane 1) or the control phospho-peptide AEIGVGAY*GTVYKARDPHS (SEQ. ID NO: 90), corresponding to an amino terminal peptide of human Cdk4 with a phosphotyrosine at position 17 (Y*) (lane 3). Beads were washed with RIPA buffer and bound proteins were immunoblotted with antibodies to the proteins indicated on the left of each panel. A portion of the HeLa extract (25 μg) was used as a control (lane 4). The slower migrating band in Cul1 is likely generated by the covalent attachment of a ubiquitin-like molecule, as already described for other cullins 48. **C.** One μl of in vitro translated [35S] wild type p27 (WT, lanes 1-4) or p27(T187A) mutant (T187A, lanes 5-6) were incubated for 30 minutes at 30¼C in 10 μl of kinase buffer. Where indicated, ~2.5 pmole of recombinant purified cyclin E/Cdk2 or ~1 pmole Skp2 (in Skp1/Skp2 complex) were added. Samples were then incubated with 6 μl of Protein-A beads to which antibodies to Skp2 had been covalently linked. Beads were washed with RIPA buffer and bound proteins subjected to electrophoresis and autoradiography. Lanes 1-6: Skp2-bound proteins; Lanes 7 and 8: 7.5% of the in vitro translated [35S] protein inputs.

Please replace the paragraph on page 97, from lines 3-14, with the following paragraph:

Antisense experiments were performed as described in (Yu, 1998, Proc. Natl. Acad. Sci. U. S. A. 95: 11324). Briefly, four oligodeoxynucleotides that contain a phosphorothioate backbone and C-5 propyne pyrimidines were synthesized (Keck Biotechnology Resource Laboratory at Yale University): (1) 5'-CCTGGGGGATGTTCTCA-3' (SEQ ID NO: 86) (the antisense direction of human Skp2 cDNA nucleotides 180-196); (2)

5'-GGCTTCCGGGCATTTAG-3' (SEQ ID NO: 87) [the scrambled control of (1)]; (3) 5'-CATCTGGCACGATTCCA-3' (SEQ ID NO: 88) (the antisense direction of Skp2 cDNA nucleotides 1137-1153); (4) 5'-CCGCTCATCGTATGACA-3' (~~89~~ SEQ. ID NO: 89) [the scrambled control for (3)]. The oligonucleotides were delivered into HeLa cells using Cytofectin GS (Glen Research) according to the manufacturers instructions. The cells were then harvested between 16 and 18 hours postransfection.

Please replace the paragraph on page 103, from lines 2-24, with the following paragraph:

The factor from fraction 1 is purified. FIG. 46A shows the last step of purification on a gel filtration column. The peak of active material from the MonoS step was applied to a Superdex 75 HR 10/30 column (Pharmacia) equilibrated with 20 mM Tris-HCl (pH 7.2), 150 mM NaCl, 1 mM DTT and 01% Brij-35. Samples of 0.5 ml were collected at a flow rate of 0.4 ml/min. Column fractions were concentrated to a volume of 50 μl by centrifuge ultrafiltration (Centricon-10, Amicon). Samples of 0.004 μl of column fractions were assayed for activity to stimulate p27-ubiquitin ligation. Results were quantified by phosphorimager analysis and were expressed as the percentage of ^{35}S-p27 converted to ubiquitin conjugates. Arrows at top indicate the elution position of molecular mass marker proteins (kDa). Activity eluted as a sharp peak at an apparent molecular mass of approx. 10 kDa. Electrophoresis of samples of 2.5 μl from the indicated fractions of the Superdex 75 column on a 16% polyacrylamide-SDS gel and silver staining of column fractions show a single protein of approx. 10 kDa (FIG. 46B). Numbers on the right indicate the migration position of molecular mass marker proteins (kDa). Elution of the ~10 kDa protein peak coincided with the elution of the peak of activity in fractions 27-28. However, a similar-sized protein continues to be eluted in fractions 30-31, where activity declines markedly. To identify the protein(s), samples from fraction 28 (peak of activity) and fraction 31, subsequent to the peak of activity, are subjected to mass spectrometric sequencing of tryptic peptides. A tryptic peptide of the sequence QIYYSDKYDDEEFEYR (SEQ. ID. NO: 92), corresponding to amino acid residues 5-20 of human Cks1, is detected in the ~10 kDa protein of both fractions. The reason for the difference in the activity of the Cks1 protein in these different fractions is not known. Possibly, the Cks1 protein in fraction 31 is a denatured ~~conformer~~ conformer that may have altered exclusion properties in the gel filtration column.